

Figure S4. Thiamine and Biotin Metabolism in *Hormoscilla* vs *S. elongatus* and *Moorea producens*

These metabolic maps were made using ec2kegg and follow the same coloring scheme: Yellow boxes indicate the corresponding EC number is present in both reference and query genomes. Green boxes are EC numbers only found in the reference genome (*S. elongatus* PCC 7942 in S4a and *M. producens* in S4b). Figure S4a: Both GUM007_hs and GUM202_hs genomes appear to be lacking the three enzymes involved in the last step of thiamine biosynthesis (ECs 3.1.3.1, 3.1.3.2, and 3.1.3.100, red box). Figure S4b: The biotin pathway appears incomplete in both *M. producens* and *Hormoscilla*. Putative homologues of BioK, which can replace BioH in pimeloyl-CoA biosynthesis, were found in *M. producens* and *Hormoscilla*. However, no homologues of BioA (ECs 2.6.1.62 and 2.6.1.105, red box) have been found in either species.